



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Eaton, Dan L.
de Sauvage, Frederic J.
- (ii) TITLE OF INVENTION: MPL LIGAND
- 10 (iii) NUMBER OF SEQUENCES: 30
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
15 (C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080
- 20 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/422548
(B) FILING DATE: 13-Apr-1995
30 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/223263
(B) FILING DATE: 04-APR-1994
- 35 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994
- (vii) PRIOR APPLICATION DATA:
40 (A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994
- (vii) PRIOR APPLICATION DATA:
45 (A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 03-JAN-1994
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Winter, Daryl B.
50 (B) REGISTRATION NUMBER: 32,637
(C) REFERENCE/DOCKET NUMBER: P0871P3D1
- (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-1249
 (B) TELEFAX: 415/952-9881
 (C) TELEX: 910/371-7168

5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 353 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15	Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr	-21 -20	-15	-10
	Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu	-5	1	5
20	Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser	10	15	20
	Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val	25	30	35
25	Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln	40	45	50
30	Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu	55	60	65
	Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr	70	75	80
35	Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu	85	90	95
	Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro	100	105	110
40	Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu	115	120	125
45	Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu	130	135	140
	Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr	145	150	155
50	Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu	160	165	170

	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser	
	175					180					185					
5	Ala	Arg	Thr	Thr	Gly	Ser	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	
	190					195					200					
	Arg	Ala	Lys	Ile	Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	
	205					210					215					
10	Asp	Gln	Ile	Pro	Gly	Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	
	220					225					230					
	Gly	Thr	Arg	Gly	Leu	Phe	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	
	235					240					245					
15	Ala	Pro	Asp	Ile	Ser	Ser	Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	
	250					255					260					
	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	Ser	Pro	Ser	Pro	Thr	His	Pro	Pro	
20	265					270					275					
	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	Pro	Leu	Pro	Pro	Thr	Leu	Pro	Thr	
	280					285					290					
25	Pro	Val	Val	Gln	Leu	His	Pro	Leu	Leu	Pro	Asp	Pro	Ser	Ala	Pro	
	295					300					305					
	Thr	Pro	Thr	Pro	Thr	Ser	Pro	Leu	Leu	Asn	Thr	Ser	Tyr	Thr	His	
	310					315					320					
30	Ser	Gln	Asn	Leu	Ser	Gln	Glu	Gly								
	325					330		332								

(2) INFORMATION FOR SEQ ID NO:2:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 1795 base pairs
	(B) TYPE: Nucleic Acid
	(C) STRANDEDNESS: Single
40	(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

45	TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50
	CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100
	CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150
50	CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200

	GACACCCCGG	CCAGA		ATG	GAG	CTG	ACT	GAA	TTG	CTC	CTC	239		
				Met	Glu	Leu	Thr	Glu	Leu	Leu	Leu			
				-21	-20					-15				
5	GTG	GTC	ATG	CTT	CTC	CTA	ACT	GCA	AGG	CTA	ACG	CTG	TCC	278
	Val	Val	Met	Leu	Leu	Leu	Thr	Ala	Arg	Leu	Thr	Leu	Ser	
				-10					-5					
10	AGC	CCG	GCT	CCT	CCT	GCT	TGT	GAC	CTC	CGA	GTC	CTC	AGT	317
	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	
	1				5					10				
15	AAA	CTG	CTT	CGT	GAC	TCC	CAT	GTC	CTT	CAC	AGC	AGA	CTG	356
	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	
		15					20					25		
20	AGC	CAG	TGC	CCA	GAG	GTT	CAC	CCT	TTG	CCT	ACA	CCT	GTC	395
	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	
				30					35					
25	CTG	CTG	CCT	GCT	GTG	GAC	TTT	AGC	TTG	GGA	GAA	TGG	AAA	434
	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	
	40					45					50			
30	ACC	CAG	ATG	GAG	GAG	ACC	AAG	GCA	CAG	GAC	ATT	CTG	GGA	473
	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	
			55					60					65	
35	GCA	GTG	ACC	CTT	CTG	CTG	GAG	GGA	GTG	ATG	GCA	GCA	CGG	512
	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	
					70					75				
40	GGA	CAA	CTG	GGA	CCC	ACT	TGC	CTC	TCA	TCC	CTC	CTG	GGG	551
	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	
		80					85					90		
45	CAG	CTT	TCT	GGA	CAG	GTC	CGT	CTC	CTC	CTT	GGG	GCC	CTG	590
	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	
				95					100					
50	CAG	AGC	CTC	CTT	GGA	ACC	CAG	CTT	CCT	CCA	CAG	GGC	AGG	629
	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	
	105					110					115			
55	ACC	ACA	GCT	CAC	AAG	GAT	CCC	AAT	GCC	ATC	TTC	CTG	AGC	668
	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	
			120					125					130	
60	TTC	CAA	CAC	CTG	CTC	CGA	GGA	AAG	GTG	CGT	TTC	CTG	ATG	707
	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	
					135					140				

	CTT	GTA	GGA	GGG	TCC	ACC	CTC	TGC	GTC	AGG	CGG	GCC	CCA	746
	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala	Pro	
	145						150					155		
5	CCC	ACC	ACA	GCT	GTC	CCC	AGC	AGA	ACC	TCT	CTA	GTC	CTC	785
	Pro	Thr	Thr	Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	
				160					165					
10	ACA	CTG	AAC	GAG	CTC	CCA	AAC	AGG	ACT	TCT	GGA	TTG	TTG	824
	Thr	Leu	Asn	Glu	Leu	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	
	170					175					180			
15	GAG	ACA	AAC	TTC	ACT	GCC	TCA	GCC	AGA	ACT	ACT	GGC	TCT	863
	Glu	Thr	Asn	Phe	Thr	Ala	Ser	Ala	Arg	Thr	Thr	Gly	Ser	
			185					190					195	
20	GGG	CTT	CTG	AAG	TGG	CAG	CAG	GGA	TTC	AGA	GCC	AAG	ATT	902
	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	Ile	
				200						205				
25	CCT	GGT	CTG	CTG	AAC	CAA	ACC	TCC	AGG	TCC	CTG	GAC	CAA	941
	Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	Asp	Gln	
		210					215					220		
30	ATC	CCC	GGA	TAC	CTG	AAC	AGG	ATA	CAC	GAA	CTC	TTG	AAT	980
	Ile	Pro	Gly	Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	
				225					230					
35	GGA	ACT	CGT	GGA	CTC	TTT	CCT	GGA	CCC	TCA	CGC	AGG	ACC	1019
	Gly	Thr	Arg	Gly	Leu	Phe	Pro	Gly	Pro	Ser	Arg	Arg	Thr	
	235					240					245			
40	CTA	GGA	GCC	CCG	GAC	ATT	TCC	TCA	GGA	ACA	TCA	GAC	ACA	1058
	Leu	Gly	Ala	Pro	Asp	Ile	Ser	Ser	Gly	Thr	Ser	Asp	Thr	
			250					255					260	
45	GGC	TCC	CTG	CCA	CCC	AAC	CTC	CAG	CCT	GGA	TAT	TCT	CCT	1097
	Gly	Ser	Leu	Pro	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	Ser	Pro	
				265						270				
50	TCC	CCA	ACC	CAT	CCT	CCT	ACT	GGA	CAG	TAT	ACG	CTC	TTC	1136
	Ser	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	
		275					280					285		
55	CCT	CTT	CCA	CCC	ACC	TTG	CCC	ACC	CCT	GTG	GTC	CAG	CTC	1175
	Pro	Leu	Pro	Pro	Thr	Leu	Pro	Thr	Pro	Val	Val	Gln	Leu	
				290					295					
60	CAC	CCC	CTG	CTT	CCT	GAC	CCT	TCT	GCT	CCA	ACG	CCC	ACC	1214
	His	Pro	Leu	Leu	Pro	Asp	Pro	Ser	Ala	Pro	Thr	Pro	Thr	
	300					305					310			

CCT ACC AGC CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC 1253
 Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His Ser
 315 320 325

5 CAG AAT CTG TCT CAG GAA GGG T AAGGT TCTCAGACAC 1290
 Gln Asn Leu Ser Gln Glu Gly
 330 332

10 TGCCGACATC AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC 1340
 CCTGGGAGAC AACTGGACAA GATTTCCTAC TTTCTCCTGA AACCCAAAGC 1390
 CCTGGTAAAA GGGATACACA GGACTGAAAA GGGAATCATT TTCTACTGTA 1440
 15 CATTATAAAC CTTCAGAAGC TATTTTTTTTA AGCTATCAGC AATACTCATC 1490
 AGAGCAGCTA GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG 1540
 ATTCTCTACA TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG 1590
 20 CCTGGCAGTT GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA 1640
 AAGGGTAATT TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCATCC 1690
 25 CCTTTACTAT CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC 1740
 TTTACTCTTG AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA 1790
 AAAAA 1795

30 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 35 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

40 Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
 -16 -15 -10 -5
 Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
 1 5 10
 45 Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
 15 20 25 26

50 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs

(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50

10 CACCTCTCCT CATCTAAGAA TTG CTC CTC GTG GTC ATG CTT 91
Leu Leu Leu Val Val Met Leu
-16 -15 -10

15 CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT CCT 130
Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro
-5 1

20 CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT 169
Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg
5 10 15

GAC TCC CAT GTC CTT CAC AGC AGA CTG GTGA GAACTCCCAA 210
Asp Ser His Val Leu His Ser Arg Leu
20 25 26

25 CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA 260

GACACCATCA CTCCTCTAA CTCCTTGACC CAATGACTAT TCTTCCCATA 310

30 TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT 360
ACAGCCCGCA TTATAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:5:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

45 TCTAGACGAG AGCTTTTAAA TGC GGGCTGT ATTGTGAAGA ATAATTCTTG 50

TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100

50 GGTCAAGGAG TTAGAGGAAG TGATGGTGTC TTCCTGGGAG TATGGGTGTC 150

TTACCAGTTA CGCGGATAAA GGGGATAATG TTGGGAGTTC TCACCAGTCT 200

GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250
 CACAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300
 5 AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350
 ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	1	5	10	15
Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	20	25	30	
Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	35	40	45	
Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	50	55	60	
Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	65	70	75	
Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	80	85	90	
Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	95	100	105	
Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	110	115	120	
His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	125	130	135	
Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	140	145	150	
Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr	Ala	Val	Pro	Ser	Arg	Thr	155	160	165	
Ser	Leu	Val	Leu	Thr	Leu	Asn	Glu	Leu	Pro	Asn	Arg	Thr	Ser	Gly	170	175	180	

	Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser	Ala	Arg	Thr	Thr	Gly	Ser	185	190	195
5	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	Ile	Pro	Gly	200	205	210
	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	Asp	Gln	Ile	Pro	Gly	Tyr	215	220	225
10	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	Gly	Thr	Arg	Gly	Leu	Phe	230	235	240
	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	Ala	Pro	Asp	Ile	Ser	Ser	245	250	255
15	Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	Pro	Asn	Leu	Gln	Pro	Gly	260	265	270
20	Tyr	Ser	Pro	Ser	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr	Thr	Leu	275	280	285
	Phe	Pro	Leu	Pro	Pro	Thr	Leu	Pro	Thr	Pro	Val	Val	Gln	Leu	His	290	295	300
25	Pro	Leu	Leu	Pro	Asp	Pro	Ser	Ala	Pro	Thr	Pro	Thr	Pro	Thr	Ser	305	310	315
	Pro	Leu	Leu	Asn	Thr	Ser	Tyr	Thr	His	Ser	Gln	Asn	Leu	Ser	Gln	320	325	330
30	Glu	Gly														332		

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	1	5	10	15
45	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	20	25	30	
50	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	35	40	45	
	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala				

	50	55	60
	Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu		
	65	70	75
5	Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro		
	80	85	90
10	Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu		
	95	100	105
	Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser		
	110	115	120
15	Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala		
	125	130	135
	Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg		
	140	145	150
20	Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp		
	155	160	165
25	Arg		
	166		

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1443 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50

AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100

ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGA ATG GAG 143

Met Glu

-21 -20

CTG ACT GAT TTG CTC CTG GCG GCC ATG CTT CTT GCA GTG 182

Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val

-15 -10

GCA AGA CTA ACT CTG TCC AGC CCC GTA GCT CCT GCC TGT 221

Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys

-5 1 5

	GAC	CCC	AGA	CTC	CTA	AAT	AAA	CTG	CTG	CGT	GAC	TCC	CAC	260
	Asp	Pro	Arg	Leu	Leu	Asn	Lys	Leu	Leu	Arg	Asp	Ser	His	
			10					15					20	
5	CTC	CTT	CAC	AGC	CGA	CTG	AGT	CAG	TGT	CCC	GAC	GTC	GAC	299
	Leu	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Asp	Val	Asp	
					25					30				
10	CCT	TTG	TCT	ATC	CCT	GTT	CTG	CTG	CCT	GCT	GTG	GAC	TTT	338
	Pro	Leu	Ser	Ile	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	
		35					40					45		
15	AGC	CTG	GGA	GAA	TGG	AAA	ACC	CAG	ACG	GAA	CAG	AGC	AAG	377
	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Thr	Glu	Gln	Ser	Lys	
				50				55						
20	GCA	CAG	GAC	ATT	CTA	GGG	GCA	GTG	TCC	CTT	CTA	CTG	GAG	416
	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Ser	Leu	Leu	Leu	Glu	
	60					65					70			
25	GGA	GTG	ATG	GCA	GCA	CGA	GGA	CAG	TTG	GAA	CCC	TCC	TGC	455
	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Glu	Pro	Ser	Cys	
			75				80						85	
30	CTC	TCA	TCC	CTC	CTG	GGA	CAG	CTT	TCT	GGG	CAG	GTT	CGC	494
	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	
					90					95				
35	CTC	CTC	TTG	GGG	GCC	CTG	CAG	GGC	CTC	CTA	GGA	ACC	CAG	533
	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Gly	Leu	Leu	Gly	Thr	Gln	
		100					105					110		
40	GGC	AGG	ACC	ACA	GCT	CAC	AAG	GAC	CCC	AAT	GCC	CTC	TTC	572
	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Leu	Phe	
				115					120					
45	TTG	AGC	TTG	CAA	CAA	CTG	CTT	CGG	GGA	AAG	GTG	CGC	TTC	611
	Leu	Ser	Leu	Gln	Gln	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	
	125					130					135			
50	CTG	CTT	CTG	GTA	GAA	GGT	CCC	ACC	CTC	TGT	GTC	AGA	CGG	650
	Leu	Leu	Leu	Val	Glu	Gly	Pro	Thr	Leu	Cys	Val	Arg	Arg	
			140				145						150	
55	ACC	CTG	CCA	ACC	ACA	GCT	GTC	CCA	AGC	AGT	ACT	TCT	CAA	689
	Thr	Leu	Pro	Thr	Thr	Ala	Val	Pro	Ser	Ser	Thr	Ser	Gln	
					155					160				
60	CTC	CTC	ACA	CTA	AAC	AAG	TTC	CCA	AAC	AGG	ACT	TCT	GGA	728
	Leu	Leu	Thr	Leu	Asn	Lys	Phe	Pro	Asn	Arg	Thr	Ser	Gly	
		165					170					175		

	TTG	TTG	GAG	ACG	AAC	TTC	AGT	GTC	ACA	GCC	AGA	ACT	GCT	767
	Leu	Leu	Glu	Thr	Asn	Phe	Ser	Val	Thr	Ala	Arg	Thr	Ala	
				180					185					
5	GGC	CCT	GGA	CTT	CTG	AGC	AGG	CTT	CAG	GGA	TTC	AGA	GTC	806
	Gly	Pro	Gly	Leu	Leu	Ser	Arg	Leu	Gln	Gly	Phe	Arg	Val	
	190					195					200			
10	AAG	ATT	ACT	CCT	GGT	CAG	CTA	AAT	CAA	ACC	TCC	AGG	TCC	845
	Lys	Ile	Thr	Pro	Gly	Gln	Leu	Asn	Gln	Thr	Ser	Arg	Ser	
			205					210					215	
15	CCA	GTC	CAA	ATC	TCT	GGA	TAC	CTG	AAC	AGG	ACA	CAC	GGA	884
	Pro	Val	Gln	Ile	Ser	Gly	Tyr	Leu	Asn	Arg	Thr	His	Gly	
					220					225				
20	CCT	GTG	AAT	GGA	ACT	CAT	GGG	CTC	TTT	GCT	GGA	ACC	TCA	923
	Pro	Val	Asn	Gly	Thr	His	Gly	Leu	Phe	Ala	Gly	Thr	Ser	
		230					235					240		
25	CTT	CAG	ACC	CTG	GAA	GCC	TCA	GAC	ATC	TCG	CCC	GGA	GCT	962
	Leu	Gln	Thr	Leu	Glu	Ala	Ser	Asp	Ile	Ser	Pro	Gly	Ala	
				245					250					
30	TTC	AAC	AAA	GGC	TCC	CTG	GCA	TTC	AAC	CTC	CAG	GGT	GGA	1001
	Phe	Asn	Lys	Gly	Ser	Leu	Ala	Phe	Asn	Leu	Gln	Gly	Gly	
	255					260					265			
35	CTT	CCT	CCT	TCT	CCA	AGC	CTT	GCT	CCT	GAT	GGA	CAC	ACA	1040
	Leu	Pro	Pro	Ser	Pro	Ser	Leu	Ala	Pro	Asp	Gly	His	Thr	
								275					280	
40	CCC	TTC	CCT	CCT	TCA	CCT	GCC	TTG	CCC	ACC	ACC	CAT	GGA	1079
	Pro	Phe	Pro	Pro	Ser	Pro	Ala	Leu	Pro	Thr	Thr	His	Gly	
					285						290			
45	TCT	CCA	CCC	CAG	CTC	CAC	CCC	CTG	TTT	CCT	GAC	CCT	TCC	1118
	Ser	Pro	Pro	Gln	Leu	His	Pro	Leu	Phe	Pro	Asp	Pro	Ser	
		295					300					305		
50	ACC	ACC	ATG	CCT	AAC	TCT	ACC	GCC	CCT	CAT	CCA	GTC	ACA	1157
	Thr	Thr	Met	Pro	Asn	Ser	Thr	Ala	Pro	His	Pro	Val	Thr	
				310					315					
55	ATG	TAC	CCT	CAT	CCC	AGG	AAT	TTG	TCT	CAG	GAA	ACA	TAGCGC	1199
	Met	Tyr	Pro	His	Pro	Arg	Asn	Leu	Ser	Gln	Glu	Thr		
	320					325					330	331		
60	G	GGCACTGGCC	CAGTGAGCGT	CTGCAGCTTC	TCTCGGGGAC	1240								
65	AAGCTTCCCC	AGGAAGGCTG	AGAGGCAGCT	GCATCTGCTC	CAGATGTTCT	1290								

GCTTTCACCT AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT 1340
 AAAATTTTAG GAGCTATTTT TTTTAACT ATCAGCAATA TTCATCAGAG 1390
 5 CAGCTAGCGA TCTTTGGTCT ATTTTCGGTA TAAATTTGAA AATCACTAAT 1440
 TCT 1443

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Glu	Leu	Thr	Asp	Leu	Leu	Leu	Ala	Ala	Met	Leu	Leu	Ala	Val
-21	-20					-15					-10			
Ala	Arg	Leu	Thr	Leu	Ser	Ser	Pro	Val	Ala	Pro	Ala	Cys	Asp	Pro
	-5					1				5				
Arg	Leu	Leu	Asn	Lys	Leu	Leu	Arg	Asp	Ser	His	Leu	Leu	His	Ser
10					15					20				
Arg	Leu	Ser	Gln	Cys	Pro	Asp	Val	Asp	Pro	Leu	Ser	Ile	Pro	Val
25					30					35				
Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln
40					45					50				
Thr	Glu	Gln	Ser	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Ser	Leu
55					60					65				
Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Glu	Pro	Ser
70					75					80				
Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu
85					90					95				
Leu	Leu	Gly	Ala	Leu	Gln	Gly	Leu	Leu	Gly	Thr	Gln	Gly	Arg	Thr
100					105					110				
Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Leu	Phe	Leu	Ser	Leu	Gln	Gln
115					120					125				
Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Leu	Leu	Val	Glu	Gly	Pro
130					135					140				
Thr	Leu	Cys	Val	Arg	Arg	Thr	Leu	Pro	Thr	Thr	Ala	Val	Pro	Ser
145					150					155				

	Ser	Thr	Ser	Gln	Leu	Leu	Thr	Leu	Asn	Lys	Phe	Pro	Asn	Arg	Thr
	160					165					170				
5	Ser	Gly	Leu	Leu	Glu	Thr	Asn	Phe	Ser	Val	Thr	Ala	Arg	Thr	Ala
	175					180					185				
	Gly	Pro	Gly	Leu	Leu	Ser	Arg	Leu	Gln	Gly	Phe	Arg	Val	Lys	Ile
	190					195					200				
10	Thr	Pro	Gly	Gln	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Pro	Val	Gln	Ile
	205					210					215				
	Ser	Gly	Tyr	Leu	Asn	Arg	Thr	His	Gly	Pro	Val	Asn	Gly	Thr	His
	220					225					230				
15	Gly	Leu	Phe	Ala	Gly	Thr	Ser	Leu	Gln	Thr	Leu	Glu	Ala	Ser	Asp
	235					240					245				
	Ile	Ser	Pro	Gly	Ala	Phe	Asn	Lys	Gly	Ser	Leu	Ala	Phe	Asn	Leu
20	250					255					260				
	Gln	Gly	Gly	Leu	Pro	Pro	Ser	Pro	Ser	Leu	Ala	Pro	Asp	Gly	His
	265					270					275				
25	Thr	Pro	Phe	Pro	Pro	Ser	Pro	Ala	Leu	Pro	Thr	Thr	His	Gly	Ser
	280					285					290				
	Pro	Pro	Gln	Leu	His	Pro	Leu	Phe	Pro	Asp	Pro	Ser	Thr	Thr	Met
	295					300					305				
30	Pro	Asn	Ser	Thr	Ala	Pro	His	Pro	Val	Thr	Met	Tyr	Pro	His	Pro
	310					315					320				
	Arg	Asn	Leu	Ser	Gln	Glu	Thr								
35	325					330	331								

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 331 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

45	Ser	Pro	Val	Ala	Pro	Ala	Cys	Asp	Pro	Arg	Leu	Leu	Asn	Lys	Leu
	1				5				10						15
	Leu	Arg	Asp	Ser	His	Leu	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro
50					20				25						30
	Asp	Val	Asp	Pro	Leu	Ser	Ile	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp

				35					40					45	
	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Thr	Glu	Gln	Ser	Lys	Ala
					50					55					60
5	Gln	Asp	Ile	Leu	Gly	Ala	Val	Ser	Leu	Leu	Leu	Glu	Gly	Val	Met
					65					70					75
10	Ala	Ala	Arg	Gly	Gln	Leu	Glu	Pro	Ser	Cys	Leu	Ser	Ser	Leu	Leu
					80					85					90
	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln
					95					100					105
15	Gly	Leu	Leu	Gly	Thr	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro
					110					115					120
	Asn	Ala	Leu	Phe	Leu	Ser	Leu	Gln	Gln	Leu	Leu	Arg	Gly	Lys	Val
					125					130					135
20	Arg	Phe	Leu	Leu	Leu	Val	Glu	Gly	Pro	Thr	Leu	Cys	Val	Arg	Arg
					140					145					150
25	Thr	Leu	Pro	Thr	Thr	Ala	Val	Pro	Ser	Ser	Thr	Ser	Gln	Leu	Leu
					155					160					165
	Thr	Leu	Asn	Lys	Phe	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr
					170					175					180
30	Asn	Phe	Ser	Val	Thr	Ala	Arg	Thr	Ala	Gly	Pro	Gly	Leu	Leu	Ser
					185					190					195
	Arg	Leu	Gln	Gly	Phe	Arg	Val	Lys	Ile	Thr	Pro	Gly	Gln	Leu	Asn
					200					205					210
35	Gln	Thr	Ser	Arg	Ser	Pro	Val	Gln	Ile	Ser	Gly	Tyr	Leu	Asn	Arg
					215					220					225
40	Thr	His	Gly	Pro	Val	Asn	Gly	Thr	His	Gly	Leu	Phe	Ala	Gly	Thr
					230					235					240
	Ser	Leu	Gln	Thr	Leu	Glu	Ala	Ser	Asp	Ile	Ser	Pro	Gly	Ala	Phe
					245					250					255
45	Asn	Lys	Gly	Ser	Leu	Ala	Phe	Asn	Leu	Gln	Gly	Gly	Leu	Pro	Pro
					260					265					270
	Ser	Pro	Ser	Leu	Ala	Pro	Asp	Gly	His	Thr	Pro	Phe	Pro	Pro	Ser
					275					280					285
50	Pro	Ala	Leu	Pro	Thr	Thr	His	Gly	Ser	Pro	Pro	Gln	Leu	His	Pro
					290					295					300

Leu Phe Pro Asp Pro Ser Thr Thr Met Pro Asn Ser Thr Ala Pro
305 310 315

His Pro Val Thr Met Tyr Pro His Pro Arg Asn Leu Ser Gln Glu
320 325 330

Thr
331

10 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Asp Xaa Val Leu His Gly Arg Leu
20 25 26

25 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Asp His Val Leu His Gly Arg
20 25

40 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Arg Leu Leu Asn Lys Leu Leu Arg
1 5 9

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCNGCNCCNC CNGCNTGYGA 20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

NCCRTGNARN ACRTGRTCRT C 21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50
TGACCACGTT CAGCACGGC 69

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50
CGACCACGTC CATCACGGC 69

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50
CGATCATGTC TATCACGGT 69

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

(2) INFORMATION FOR SEQ ID NO:22:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAGTCTGCCG TGAAGGACAT GG 22

15

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

20

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

25

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15

Leu Arg Asp Ser His Val Leu His
20 23

30

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

35

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

40

Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro
1 5 10 15

Val Leu Leu Pro Ala Val Asp Phe
20 23

45

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

50

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln
1 5 10 15

Asp Ile Leu Gly Ala Val Thr Leu
20 23

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
1 5 10 15

Cys Leu Ser Ser Leu
20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu
1 5 10 15

Gln Ser Leu
18

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys
1 5 10 15

Asp Pro Asn Ala Ile Phe
20 21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
1 5 10 15

Leu Val Gly Gly Ser Thr Leu Cys Val Arg
20 25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Asp His Val Leu His Gly Arg
20 25